

SEQUENCE LISTING

<110> University of Rochester

Chang, Chawnshang

<120> Non-androgen Dependent Roles for
Androgen Receptor and Non-androgen Related Inhibitors of
Androgen Receptor

<130> 21108.0037P1

<140> Unassigned

<141> 2004-12-13

<150> 60/529,011

<151> 2003-12-12

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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1 5 10 15
Ala Ile Ser Ala Val Val Asp Asn Tyr Ile Arg Ser Arg Arg Asp Ile
20 25 30
Arg Ser Leu Pro Glu Asn Ile Gln Phe Asp Val Tyr Tyr Lys Leu Tyr
35 40 45
Gln Gln Gly Arg Leu Cys Gln Leu Gly Ser Glu Phe Cys Glu Leu Glu
50 55 60
Val Phe Ala Lys Val Leu Arg Ala Leu Asp Lys Arg His Leu Leu His
65 70 75 80
His Cys Phe Gln Ala Leu Met Asp His Gly Val Lys Val Ala Ser Val
85 90 95
Leu Ala Tyr Ser Phe Ser Arg Arg Cys Ser Tyr Ile Ala Glu Ser Asp
100 105 110
Ala Ala Val Lys Glu Lys Ala Ile Gln Val Gly Phe Val Leu Gly Gly
115 120 125
Phe Leu Ser Asp Ala Gly Trp Tyr Ser Asp Ala Glu Lys Val Phe Leu
130 135 140
Ser Cys Leu Gln Leu Cys Thr Leu His Asp Glu Met Leu His Trp Phe
145 150 155 160
Arg Ala Val Glu Cys Cys Val Arg Leu Leu His Val Arg Asn Gly Asn
165 170 175
Cys Lys Tyr His Leu Gly Glu Glu Thr Phe Lys Leu Ala Gln Thr Tyr
180 185 190
Met Asp Lys Leu Ser Lys His Gly Gln Gln Ala Asn Lys Ala Ala Leu
195 200 205
Tyr Gly Glu Leu Cys Ala Leu Leu Phe Ala Lys Ser His Tyr Asp Glu
210 215 220

Ala Tyr Lys Trp Cys Ile Glu Ala Met Lys Glu Ile Thr Ala Gly Leu
 225 230 235 240
 Pro Val Lys Val Val Asp Val Leu Arg Gln Ala Ser Lys Ala Cys
 245 250 255
 Val Val Lys Arg Glu Phe Lys Lys Ala Glu Gln Leu Ile Lys His Ala
 260 265 270
 Val Tyr Leu Ala Arg Asp His Phe Gly Ser Lys His Pro Lys Tyr Ser
 275 280 285
 Asp Thr Leu Leu Asp Tyr Gly Phe Tyr Leu Leu Asn Val Asp Asn Ile
 290 295 300
 Cys Gln Ser Val Ala Ile Tyr Gln Ala Ala Leu Asp Ile Arg Gln Ser
 305 310 315 320
 Val Phe Gly Gly Lys Asn Ile His Val Ala Thr Ala His Glu Asp Leu
 325 330 335
 Ala Tyr Ser Ser Tyr Val His Gln Tyr Ser Ser Gly Lys Phe Asp Asn
 340 345 350
 Ala Leu Phe His Ala Glu Arg Ala Ile Gly Ile Ile Thr His Ile Leu
 355 360 365
 Pro Glu Asp His Leu Leu Leu Ala Ser Ser Lys Arg Val Lys Ala Leu
 370 375 380
 Ile Leu Glu Glu Ile Ala Ile Asp Cys His Asn Lys Glu Thr Glu Gln
 385 390 395 400
 Arg Leu Leu Gln Glu Ala His Asp Leu His Leu Ser Ser Leu Gln Leu
 405 410 415
 Ala Lys Lys Ala Phe Gly Glu Phe Asn Val Gln Thr Ala Lys His Tyr
 420 425 430
 Gly Asn Leu Gly Arg Leu Tyr Gln Ser Met Arg Lys Phe Lys Glu Ala
 435 440 445
 Glu Glu Met His Ile Lys Ala Ile Gln Ile Lys Glu Gln Leu Leu Gly
 450 455 460
 Gln Glu Asp Tyr Glu Val Ala Leu Ser Val Gly His Leu Ala Ser Leu
 465 470 475 480
 Tyr Asn Tyr Asp Met Asn Gln Tyr Glu Asn Ala Glu Lys Leu Tyr Leu
 485 490 495
 Arg Ser Ile Ala Ile Gly Lys Lys Leu Phe Gly Glu Gly Tyr Ser Gly
 500 505 510
 Leu Glu Tyr Asp Tyr Arg Gly Leu Ile Lys Leu Tyr Asn Ser Ile Gly
 515 520 525
 Asn Tyr Glu Lys Val Phe Glu Tyr His Asn Val Leu Ser Asn Trp Asn
 530 535 540
 Arg Leu Arg Asp Arg Gln Tyr Ser Val Thr Asp Ala Leu Glu Asp Val
 545 550 555 560
 Ser Thr Ser Pro Gln Ser Thr Glu Glu Val Val Gln Ser Phe Leu Ile
 565 570 575
 Ser Gln Asn Val Glu Gly Pro Ser Cys
 580 585

<210> 2
 <211> 1758
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 2
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 gtcgtggaca actacatccg ctcccgccga gacatccgct ccttgcggga gaacatccag 120
 tttgatgttt actacaagct ttaccaacag ggacgcttat gtcaactggg cagtgaattt 180
 tgtgaattgg aagttttgc taaagtactg agagcttgg ataaaagaca tttgcttcat 240

<210> 3
<211> 919
<212> PRT
<213> Artificial Sequence

<220> |
<223> Description of Artificial Sequence:/note =
synthetic construct

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<400> 3
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
      5          10          15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
      20          25          30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
      35          40          45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
      50          55          60
Gln Glu Thr
      65          70          75          80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
      85          90          95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
      100         105         110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
      115         120         125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
      130         135         140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
      145         150         155         160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
      165         170         175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
      180         185         190

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Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
 195 200 205
 Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
 210 215 220
 Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
 225 230 235 240
 Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
 245 250 255
 Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
 260 265 270
 Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
 275 280 285
 Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
 290 295 300
 Ala Glu Tyr Ser Pro Phe Lys Gly Tyr Thr Lys Gly Leu Glu Gly
 305 310 315 320
 Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Gly Ser Ser Gly Thr
 325 330 335
 Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
 340 345 350
 Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
 355 360 365
 Leu Ala Gly Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
 370 375 380
 Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
 385 390 395 400
 Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
 405 410 415
 Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser
 420 425 430
 Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
 435 440 445
 Gly
 450 455 460
 Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr
 465 470 475 480
 Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe
 485 490 495
 Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro
 500 505 510
 Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp
 515 520 525
 Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp
 530 535 540
 His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu
 545 550 555 560
 Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
 565 570 575
 Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys
 580 585 590
 Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg
 595 600 605
 Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met
 610 615 620
 Thr Leu Gly Ala Arg Lys Leu Lys Leu Gly Asn Leu Lys Leu Gln
 625 630 635 640
 Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr
 645 650 655
 Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile
 660 665 670

Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
 675 680 685
 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
 690 695 700
 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
 705 710 715 720
 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
 725 730 735
 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
 740 745 750
 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
 755 760 765
 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
 770 775 780
 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
 785 790 795 800
 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Phe Ser Ile Ile
 805 810 815
 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
 820 825 830
 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
 835 840 845
 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
 850 855 860
 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
 865 870 875 880
 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
 885 890 895
 Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
 900 905 910
 Pro Ile Tyr Phe His Thr Gln
 915

<210> 4
 <211> 4321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 aagggacgca ccacgcccagc cccagcccg ctccagcgcac agccaaacgcc ttttgcagcg 180
 cggccgcttc gaagccggc cccggagctg ccctttcctc ttccgtgaag tttttaaaag 240
 ctgctaaaga ctcggagaa gcaaggaaag tgcctggtag gactgacggc tgcctttgtc 300
 ctccctcctct ccacccccc tccccccacc ctgccttccc cccctccccc gtcttctctc 360
 cccgagctgc ctcagtccgc tactctcagc caacccccc caccaccctt ctcccccaccc 420
 gcccccccgcc ccccgtccgc ccagcgctgc cagcccgagt ttgcagagag gtaactccct 480
 ttggctgcga gccccggcgc tagctgcaca ttgcaaagaa ggctcttagg agccaggcga 540
 ctggggagcg gcttcagcac tgcagccacg acccgctgg ttagaattcc ggcggagaga 600
 accctctgtt ttcccccaact ctctctccac ctccctctgc cttcccccacc cccgagtgcgg 660
 agcagagatc aaaagatgaa aaggcagtca ggtcttcagt agccaaaaaaa caaaacaaaac 720
 aaaaacaaaa aagccgaaat aaaaagaaaa gataataact cagttcttat ttgcacctac 780
 ttcagtggac actgaatttg gaaggtggag gatttgttt ttttctttta agatctggc 840
 atctttgaa tctacccttc aagtattaag agacagactg tgagcctagc agggcagatc 900
 ttgtccacccg tgggtcttct tctgcacccg actttgaggc tggcagagcg ctttttgcgt 960
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 actaccgcatt catcacagcc tggtaactc ttctgagcaa gagaaggggaa ggcggggtaa 1080

gggaagttagg	tggaagattc	agccaagctc	aaggatggaa	gtgcagttag	ggctggaaag	1140
ggcttaccct	cgccgcgt	ccaagaccta	ccgaggagct	ttccagaatc	tgttccagag	1200
cgtgcgcgaa	gtgatccaga	accgggccc	caggcaccct	gaggccgcga	gcccgcacc	1260
tcccgccgc	agtttgcgtc	tgcgcagca	gcagcagcag	cagcagcagc	agcagcagca	1320
gcagcagcag	cagcagcagc	agcagcaaga	gactagcccc	aggcagcagc	agcagcagca	1380
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tgcgagagag	ctgcatcagt	tcactttga	cctgcttaatc	aagtccacaca	tggtgagcgt	3780
ggactttccg	gaaatgtgg	cagagatcat	ctctgtgca	gtgcccaga	tcctttctgg	3840
gaaagtcaag	cccatctatt	tccacaccca	gtgaagcatt	ggaaacccctt	tttccccacc	3900
ccagctcatg	cccccttca	gatgtcttct	gcctgttata	actctgcact	actctctgc	3960
agtgccttgg	ggaatttcc	ctattgtatgt	acagtctgtc	atgaacatgt	tcctgtattc	4020
tatttgcgtt	gttttttttt	tcttttctc	tcctttcttt	ttcttcttcc	tccttctatct	4080
aaccctccca	tggcaccc	agactttgt	tcccattgt	gctcctatct	gtgttttgaa	4140
tggtgttgc	tgcctttaaa	tctgtgtatg	tcctcatatg	gcccagtgtc	aagttgtgt	4200
tgtttacagc	actactctgt	gccagccaca	caaacgttta	tttatcttat	gccacgggaa	4260
gtttagagag	ctaagattat	ctggggaaat	caaaacaaaa	aacaagcaaa	caaaaaaaaaaa	4320
a						4321

<210> 5
 <211> 433
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

Met Ser Gly Arg Pro Arg Thr Thr Ser Phe Ala Glu Ser Cys Lys Pro
 1 5 10 15
 Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
 20 25 30
 Asp Gly Ser Lys Val Thr Val Ala Thr Pro Gly Gln Gly Pro
 35 40 45
 Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
 50 55 60
 Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
 65 70 75 80
 Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
 85 90 95
 Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
 100 105 110
 Arg Tyr Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
 115 120 125
 Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
 130 135 140
 His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
 145 150 155 160
 Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
 165 170 175
 Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Asp Pro Asp
 180 185 190
 Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
 195 200 205
 Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala
 210 215 220
 Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
 225 230 235 240
 Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
 245 250 255
 Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
 260 265 270
 Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
 275 280 285
 Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Asp
 290 295 300
 Ser Ser Gly Thr Gly His Phe Thr Ser Gly Val Arg Val Phe Arg Pro
 305 310 315 320
 Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu Leu Glu Tyr
 325 330 335
 Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala His Ser Phe
 340 345 350
 Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn Gly Arg Asp
 355 360 365
 Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser Ser Asn Pro
 370 375 380
 Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile Gln Ala Ala
 385 390 395 400
 Ala Ser Thr Pro Thr Asn Ala Thr Ala Ala Ser Asp Ala Asn Thr Gly
 405 410 415
 Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala Ser Asn Ser
 420 425 430

Thr

<210> 6
 <211> 1639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 6

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cttctgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaagaca	180
aaaggaagaa	aaggaggaaag	gaaggaaaag	gtgattcgcg	aagagagtga	tcatgtcagg	240
gccccccaga	accacccct	ttgcggagag	ctgcaagccg	gtgcagcagc	cttcagcttt	300
tggcagcatt	aaagttagca	gagacaaggaa	cggcagcaag	gtgacaacag	tggggcaac	360
tcctggcag	ggtccagaca	ggccacaaga	agtcaagctat	acagacacta	aagtgattgg	420
aatggatca	tttggtgtgg	tatataaaggc	caaacttgt	gattcaggag	aactggtcgc	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcatgagaaa	540
gctagatcac	tgtacatag	tccgattgcg	ttatttcttc	tactccagt	gtgagaagaa	600
agatgaggtc	tatctaattc	tggtgcgtgg	ctatgtccg	aaaacagtat	acagagttgc	660
cagacactat	agtcaagcc	aacagacgc	ccctgtgatt	tatgtcaagt	tgtatatgt	720
tcagctgttc	cgaagtttag	cctataatcca	ttcccttgg	atctgccc	gggatattaa	780
accgcagaac	ctcttgggg	atcctgatac	tgctgttata	aaactctgt	actttggaaag	840
tgcaaaggcag	ctggtccgag	gagaacccaa	tgtttcgat	atctgttctc	ggtactatag	900
ggcaccagag	ttgatcttt	gagccactga	ttataccct	agtatagat	tatggctgc	960
tggctgtgt	ttggctgagc	tgttactagg	acaaccaata	tttccagggg	atagtgggt	1020
ggatcagttg	gtagaaataa	tcaaggtcct	gggaaactcca	acaagggagc	aaatcagaga	1080
aatgaacccaa	aactacacag	aatttaaatt	ccctcaaatt	aaggcacatc	cttggactaa	1140
ggattcgtca	ggaacaggac	atttcacctc	aggagtgcgg	gtcttccgac	cccgaaactcc	1200
accggaggca	attgcactgt	gtagccgtct	gctggagtat	acaccaact	cccgactaac	1260
accactggaa	gcttgcac	attcattttt	tgtatgaattt	cgggacccaa	atgtcaaact	1320
accaaattggg	cgagacacac	ctgcactctt	caacttcacc	actcaagaac	tgtcaagtaa	1380
tccacccctg	gctaccatcc	ttattccctcc	tcatgtcgg	attcaagcag	ctgcttcaac	1440
ccccacaaat	gccacagcag	cgtcagatgc	taatactgg	gaccgtggac	agaccaataa	1500
tgcgttct	gcatcagctt	ccaactccac	ctgaacagtc	ccgagcagcc	agctgcacag	1560
aaaaaaccac	cagttacttg	agtgtcaactc	agcaacactg	gtcacgttt	gaaagaatat	1620
aaaaaaaaaa	aaaaaaaaaa					1639

<210> 7
 <211> 391
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 7

Met	Lys	Cys	Leu	Val	Thr	Gly	Gly	Asn	Val	Lys	Val	Leu	Gly	Lys	Ala
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Val	His	Ser	Leu	Ser	Arg	Ile	Gly	Asp	Glu	Leu	Tyr	Leu	Glu	Pro	Leu
						20			25				30		
Glu	Asp	Gly	Leu	Ser	Leu	Arg	Thr	Val	Asn	Ser	Ser	Arg	Ser	Ala	Tyr
						35			40			45			
Ala	Cys	Phe	Leu	Phe	Ala	Pro	Leu	Phe	Phe	Gln	Gln	Tyr	Gln	Ala	Ala
						50			55			60			
Thr	Pro	Gly	Gln	Asp	Leu	Leu	Arg	Cys	Lys	Ile	Leu	Met	Lys	Ser	Phe
						65			70			75			80

Leu Ser Val Phe Arg Ser Leu Ala Met Leu Glu Lys Thr Val Glu Lys
 85 90 95
 Cys Cys Ile Ser Leu Asn Gly Arg Ser Ser Arg Leu Val Val Gln Leu
 100 105 110
 His Cys Lys Phe Gly Val Arg Lys Thr His Asn Leu Ser Phe Gln Asp
 115 120 125
 Cys Glu Ser Leu Gln Ala Val Phe Asp Pro Ala Ser Cys Pro His Met
 130 135 140
 Leu Arg Ala Pro Ala Arg Val Leu Gly Glu Ala Val Leu Pro Phe Ser
 145 150 155 160
 Pro Ala Leu Ala Glu Val Thr Leu Gly Ile Gly Arg Gly Arg Val
 165 170 175
 Ile Leu Arg Ser Tyr His Glu Glu Ala Asp Ser Thr Ala Lys Ala
 180 185 190
 Met Val Thr Glu Met Cys Leu Gly Glu Glu Asp Phe Gln Gln Leu Gln
 195 200 205
 Ala Gln Glu Gly Val Ala Ile Thr Phe Cys Leu Lys Glu Phe Arg Gly
 210 215 220
 Leu Leu Ser Phe Ala Glu Ser Ala Asn Leu Asn Leu Ser Ile His Phe
 225 230 235 240
 Asp Ala Pro Gly Arg Pro Ala Ile Phe Thr Ile Lys Asp Ser Leu Leu
 245 250 255
 Asp Gly His Phe Val Leu Ala Thr Leu Ser Asp Thr Asp Ser His Ser
 260 265 270
 Gln Asp Leu Gly Ser Pro Glu Arg His Gln Pro Val Pro Gln Leu Gln
 275 280 285
 Ala His Ser Thr Pro His Pro Asp Asp Phe Ala Asn Asp Asp Ile Asp
 290 295 300
 Ser Tyr Met Ile Ala Met Glu Thr Thr Ile Gly Asn Glu Gly Ser Arg
 305 310 315 320
 Val Leu Pro Ser Ile Ser Leu Ser Pro Gly Pro Gln Pro Pro Lys Ser
 325 330 335
 Pro Gly Pro His Ser Glu Glu Glu Asp Glu Ala Glu Pro Ser Thr Val
 340 345 350
 Pro Gly Thr Pro Pro Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser
 355 360 365
 Ile Leu Ala Pro Val Arg Ser Pro Gln Gly Pro Ser Pro Val Leu Ala
 370 375 380
 Glu Asp Ser Glu Gly Glu Gly
 385 390

<210> 8
 <211> 2102
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8
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 ggcgtccac tccctgtccc gcatcgggaa cgagctctac ctggAACCTC tggaggacgg
 gctctccctc cggacggta actcctccc ctctgcctat gcctgcgttc tcttgcccc
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 cttcgaccca gcctcggtgcc cccacatgct ccgcggccca gcacgggttc tgggggaggc
 tgttctgccc ttctctcctg cactggctga agtgacgctg ggcattggcc gtggccgcag

ggtcatcctg	cgcagctacc	acgaggagga	ggcagacagc	actgc当地	ccatggtagc	660
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cacttctgc	ctcaaggaat	tccggggct	cctgagcttt	gcagagtca	caaacttga	780
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gctggacggc	cactttgtct	tggccacact	ctcagacacc	gactc当地	cccaggacct	900
gggc当地	gagcgtcacc	agccagtgc	tcagctccag	gctcacagca	caccccaccc	960
ggacgactt	gc当地	acattgactc	ttacatgatc	gccc当地	ccactatagg	1020
caatgagggc	tc当地	tc当地	ttccccc当地	c当地	agccccccaa	1080
gagccccgt	ccccactccg	aggaggaaga	tgaggctgag	ccc当地	tgcc当地	1140
tcccccaccc	aagaagttcc	gctcactgtt	cttc当地	atc当地	ctgtacgctc	1200
cccccaggc	ccc当地	tgctggc当地	agacagtgag	ggtgaaggct	gaaccaagaa	1260
cctgaagct	gtacccagag	gc当地	agacgaagcc	ccagcc当地	gc当地	1320
gtctctcagc	c当地	agaaaaggtgg	gctt当地	gctgagctgt	ttc当地	1380
ctcgaggcc	ccagctggct	gtcactgtaa	agctgtccc	c当地	gc当地	1440
ttatctcccc	acaaccccca	gccaatcagg	acttccaga	ctt当地	aactactgac	1500
gttctctac	cttatttctc	attgagcctc	aggctatact	ccagctggcc	aaggctggaa	1560
acctgtctcc	ctcaggctca	c当地	gaaaatgtca	tagtaggtgc	tgctggccccc	1620
tggtgatcca	gcttctctgc	caatcatgac	ctgttcc	ctgaa	gggcatgcat	1680
ctgggacccc	c当地	acaagtttc	ctt当地	tgatacttt	t当地	1740
ttggaattct	aagagcctt	gacccgagtg	t当地	gtt当地	ctt当地	1800
gtgccgagac	tcccaagcgg	ctctgtgcag	aagagctg	aggc当地	t当地	1860
gacggaggcc	atggcgagaa	tccagcttt	accttattc	aagagaccag	atgggttgc	1920
ccagatccg	gctgccc当地	ctgaggccaa	gc当地	agacccacga	c当地	1980
cgttccctg	agctgcagcc	t当地	gatc当地	acagtcacc	c当地	2040
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at						2102

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9
gggccccctgg atggatagt ac 22 /

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10
gtagctatcc atccaggggc c 21

<210> 11
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

ggcccccctgg atggatagct acctcgaggt agctatccat ccaggggcc

49

<210> 12
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 12
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54

<210> 13
 <211> 483
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 13
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 Gly Glu Ile Val Thr Glu Gln Gln Thr Gly Gln Lys Ile Gln Ile Val
 20 25 30
 Thr Ala Leu Asp His Asn Thr Gln Gly Lys Gln Phe Ile Leu Thr Asn
 35 40 45
 His Asp Gly Ser Thr Pro Ser Lys Val Ile Leu Ala Arg Gln Asp Ser
 50 55 60
 Thr Pro Gly Lys Val Phe Ileu Thr Pro Asp Ala Ala Gly Val Asn
 65 70 75 80
 Gln Leu Phe Phe Thr Thr Pro Asp Leu Ser Ala Gln His Leu Gln Leu
 85 90 95
 Leu Thr Asp Asn Ser Pro Asp Gln Gly Pro Asn Lys Val Phe Asp Leu
 100 105 110
 Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His Tyr Gly Ala Val
 115 120 125
 Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser Ile Arg Lys Asn
 130 135 140
 Leu Val Tyr Ser Cys Arg Gly Ser Lys Asp Cys Ile Ile Asn Lys His
 145 150 155 160
 His Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Arg Cys Ile Ala Phe
 165 170 175
 Gly Met Lys Gln Asp Ser Val Gln Cys Glu Arg Lys Pro Ile Glu Val
 180 185 190
 Ser Arg Glu Lys Ser Ser Asn Cys Ala Ala Ser Thr Glu Lys Ile Tyr
 195 200 205
 Ile Arg Lys Asp Leu Arg Ser Pro Leu Thr Ala Thr Pro Thr Phe Val
 210 215 220
 Thr Asp Ser Glu Ser Thr Arg Ser Thr Gly Leu Leu Asp Ser Gly Met
 225 230 235 240
 Phe Met Asn Ile His Pro Ser Gly Val Lys Thr Glu Ser Ala Val Leu
 245 250 255
 Met Thr Ser Asp Lys Ala Glu Ser Cys Gln Gly Asp Leu Ser Thr Leu
 260 265 270
 Ala Asn Val Val Thr Ser Leu Ala Asn Leu Gly Lys Thr Lys Asp Leu
 275 280 285

Ser Gln Asn Ser Asn Glu Met Ser Met Ile Glu Ser Leu Ser Asn Asp
 290 295 300
 Asp Thr Ser Leu Cys Glu Phe Gln Glu Met Gln Thr Asn Gly Asp Val
 305 310 315 320
 Ser Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu Asn Pro Gly Glu Ser
 325 330 335
 Thr Ala Cys Gln Ser Ser Val Ala Gly Met Glu Gly Ser Val His Leu
 340 345 350
 Ile Thr Gly Asp Ser Ser Ile Asn Tyr Thr Glu Lys Glu Gly Pro Leu
 355 360 365
 Leu Ser Asp Ser His Val Ala Phe Arg Leu Thr Met Pro Ser Pro Met
 370 375 380
 Pro Glu Tyr Leu Asn Val His Tyr Ile Gly Glu Ser Ala Ser Arg Leu
 385 390 395 400
 Leu Phe Leu Ser Met His Trp Ala Leu Ser Ile Pro Ser Phe Gln Ala
 405 410 415
 Leu Gly Gln Glu Asn Ser Ile Ser Leu Val Lys Ala Tyr Trp Asn Glu
 420 425 430
 Leu Phe Thr Leu Gly Leu Ala Gln Cys Trp Gln Val Met Asn Val Ala
 435 440 445
 Thr Ile Leu Ala Thr Phe Val Asn Cys Leu His Asn Ser Leu Gln Gln
 450 455 460
 Asp Ala Lys Val Ile Ala Leu Ile His Phe Thr Arg Arg Ala Ile
 465 470 475 480
 Thr Asp Leu

<210> 14
 <211> 596
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 14
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 Val Ala Ser Pro Gln Arg Ile Gln Ile Val Thr Asp Gln Gln Thr Gly
 20 25 30
 Gln Lys Ile Gln Ile Val Thr Ala Val Asp Ala Ser Gly Ser Pro Lys
 35 40 45
 Gln Gln Phe Ile Leu Thr Ser Pro Asp Gly Ala Gly Thr Gly Lys Val
 50 55 60
 Ile Leu Ala Ser Pro Glu Thr Ser Ser Ala Lys Gln Leu Ile Phe Thr
 65 70 75 80
 Thr Ser Asp Asn Leu Val Pro Gly Arg Ile Gln Ile Val Thr Asp Ser
 85 90 95
 Ala Ser Val Glu Arg Leu Leu Gly Lys Thr Asp Val Gln Arg Pro Gln
 100 105 110
 Val Val Glu Tyr Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His
 115 120 125
 Tyr Gly Ala Val Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser
 130 135 140
 Val Arg Lys Asn Leu Thr Tyr Ser Cys Arg Ser Asn Gln Asp Cys Ile
 145 150 155 160
 Ile Asn Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Lys Lys
 165 170 175
 Cys Leu Glu Met Gly Met Lys Met Glu Ser Val Gln Ser Glu Arg Lys
 180 185 190

Pro Phe Asp Val Gln Arg Glu Lys Pro Ser Asn Cys Ala Ala Ser Thr
 195 200 205
 Glu Lys Ile Tyr Ile Arg Lys Asp Leu Arg Ser Pro Leu Ile Ala Thr
 210 215 220
 Pro Thr Phe Val Ala Asp Lys Asp Gly Ala Arg Gln Thr Gly Leu Leu
 225 230 235 240
 Asp Pro Gly Met Leu Val Asn Ile Gln Gln Pro Leu Ile Arg Glu Asp
 245 250 255
 Gly Thr Val Leu Leu Ala Thr Asp Ser Lys Ala Glu Thr Ser Gln Gly
 260 265 270
 Ala Leu Gly Thr Leu Ala Asn Val Val Thr Ser Leu Ala Asn Leu Ser
 275 280 285
 Glu Ser Leu Asn Asn Gly Asp Thr Ser Glu Ile Gln Pro Glu Asp Gln
 290 295 300
 Ser Ala Ser Glu Ile Thr Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu
 305 310 315 320
 Asn Thr Thr Asp Ser Ser Ser Pro Ser Leu Ala Asp Gly Ile Asp
 325 330 335
 Thr Ser Gly Gly Ser Ile His Val Ile Ser Arg Asp Gln Ser Thr
 340 345 350
 Pro Ile Ile Glu Val Glu Gly Pro Leu Leu Ser Asp Thr His Val Thr
 355 360 365
 Phe Lys Leu Thr Met Pro Ser Pro Met Pro Glu Tyr Leu Asn Val His
 370 375 380
 Tyr Ile Cys Glu Ser Ala Ser Arg Leu Leu Phe Leu Ser Met His Trp
 385 390 395 400
 Ala Arg Ser Ile Pro Ala Phe Gln Ala Leu Gly Gln Asp Cys Asn Thr
 405 410 415
 Ser Leu Val Arg Ala Cys Trp Asn Glu Leu Phe Thr Leu Gly Leu Ala
 420 425 430
 Gln Cys Ala Gln Val Met Ser Leu Ser Thr Ile Leu Ala Ala Ile Val
 435 440 445
 Asn His Leu Gln Asn Ser Ile Gln Glu Asp Lys Leu Ser Gly Asp Arg
 450 455 460
 Ile Lys Gln Val Met Glu His Ile Trp Lys Leu Gln Glu Phe Cys Asn
 465 470 475 480
 Ser Met Ala Lys Leu Asp Ile Asp Gly Tyr Glu Tyr Ala Tyr Leu Lys
 485 490 495
 Ala Ile Val Leu Phe Ser Pro Asp His Pro Gly Leu Thr Ser Thr Ser
 500 505 510
 Gln Ile Glu Lys Phe Gln Glu Lys Ala Gln Met Glu Leu Gln Asp Tyr
 515 520 525
 Val Gln Lys Thr Tyr Ser Glu Asp Thr Tyr Arg Leu Ala Arg Ile Leu
 530 535 540
 Val Arg Leu Pro Ala Leu Arg Leu Met Ser Ser Asn Ile Thr Glu Glu
 545 550 555 560
 Leu Phe Phe Thr Gly Leu Ile Gly Asn Val Ser Ile Asp Ser Ile Ile
 565 570 575
 Pro Tyr Ile Leu Lys Met Glu Thr Ala Glu Tyr Asn Gly Gln Ile Thr
 580 585 590
 Gly Ala Ser Leu
 595

<210> 15

<211> 2029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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tagatcatgg caaccataga	agaaaattgca catcaaatta ttgaacaaca gatgggagag	240
attgttacag agcagcaaac	tggcagaaaa atccagattg tgacagcact tgatcataat	300
acccaaggca agcagttcat	tctgacaaat cacgacggct ctactccaag caaagtcaatt	360
ctggccaggc aagattccac	tccgggaaaa gttttcctta caactccaga tgcagcaggt	420
gtcaaccagt tattttttac	cactcctgat ctgtctgcac aacacctgca gtccttaaca	480
gataattctc cagacccaagg	accaaataag gtttttgatc ttgcgttagt atgtggagac	540
aaagcatcag gacgtcatta	tggagcagta acttgtgaag gtcgaaagg attttttaaa	600
agaagcatcc gaaaaaaattt	agtatattca tgtcgaggat caaaggattt gattattaaat	660
aagcaccacc gaaaccgctg	tcaatactgc aggttacaga gatgtattgc gtttggaaatg	720
aagcaagact ctgtccaatg	tgaaaagaaaa cccattgaag tatacggaga aaaatctcc	780
aactgtgccg cttaaacaga	aaaaatctat atccgaaagg accttcgtag cccattaact	840
gcaactccaa ctttgttaac	agatagtgaa agtacaaggat caacaggact gttagattca	900
ggaatgttca tgaatattca	tccatctgga gtaaaaaactg agtcagctgt gctgatgaca	960
tcagataagg ctgaatcatg	tcagggagat ttaagtacat tggccaatgt ggttacatca	1020
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gaaagcttaa gcaatgtatga	tacctctttt ggtgaatttc aagaaatgca gaccaacgg	1140
gatgttcaaa gggcatttga	cactcttgca aaagcattga atcctggaga gagcacagcc	1200
tgccagagct cagtagcggg	catggaaagga agtgtacacc taatcactgg agattcaagc	1260
ataaaattaca ccggaaaaaaa	ggggccactt ctcagcgatt cacatgtagc tttcaggctc	1320
accatgcctt ctccatgccc	tgagtacctg aatgtgcact acattgggaa gtctgcctcc	1380
agactgctgt tcttatcaat	gcactggca ctttcgatc cttctttcca ggctctaggg	1440
caagaaaaaca gcataatca	ggtgaaaagct tactggaatg aactttttac tcttgtctt	1500
gcccagtgt ggcaggatgt	gaatgttagca actatattag caacatttgt caattgtctt	1560
cacaatagtc ttcaacaaga	tgccaaaggta attgcagccc tcattcattt cacaagacga	1620
gcaatcaactg atttataat	gcttaactat agaatggctt atgactaccc aaaacagtgc	1680
cccatcaaca aatggggaaa	attgcctttt gagctcagga ataatttata aattggggac	1740
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actaatggat gggttttaaa	catgtccctc tacaataat taaaatctt caatgtttga	2029
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<210> 16
<211> 6450
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

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tcctgtgagg	gctgcaaggc	cttcttcaag	agaagtattc	aaggacataa	cgactatatg	1020
tgtccagcca	ccaaccagtg	caccattgat	aaaaacagga	ggaagagctg	ccaggcctgc	1080
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taaaaaagaa	aggctcatc	cagccacagg	gcagccttcc	ctgggcctt	gcttctctag	3720
cacaattatg	ggttacttcc	tttttcttaa	caaaaaagaa	tgtttgattt	cctctgggtg	3780
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aaaaatttct aggactagac gatgtataac cagctaaagc caaacaatta tacagtggaa	4620
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gatgtgactc ggttttgc cagctttgct ttgttaatg aaacacactt gtaaacctct	6360
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<210> 17
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17
cgctgttataa tccatgttggaa gtc 23

<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18
tgccttccatcc tcgtggtag 19

<210> 19

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19
 tgccttcctt ggatgtggta g

21

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 20
 cgtctgcccct atcaactttc g

21

<210> 21
 <211> 920
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 21
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 Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30
 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35 40 45
 Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
 50 55 60
 Gln
 65 70 75 80
 Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
 85 90 95
 Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
 100 105 110
 Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
 115 120 125
 Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
 130 135 140
 Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
 145 150 155 160
 Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
 165 170 175
 Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
 180 185 190
 Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
 195 200 205
 Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
 210 215 220

Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys
 225 230 235 240
 Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His
 245 250 255
 Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu
 260 265 270
 Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala
 275 280 285
 Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu
 290 295 300
 Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu
 305 310 315 320
 Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser
 325 330 335
 Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala
 340 345 350
 Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro
 355 360 365
 Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro His Pro His
 370 375 380
 Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala
 385 390 395 400
 Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly
 405 410 415
 Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser
 420 425 430
 Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly
 435 440 445
 Pro Cys Gly
 450 455 460
 Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro
 465 470 475 480
 Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp
 485 490 495
 Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val
 500 505 510
 Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met
 515 520 525
 Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg
 530 535 540
 Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys
 545 550 555 560
 Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr
 565 570 575
 Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln
 580 585 590
 Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe His
 595 600 605
 Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly
 610 615 620
 Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu
 625 630 635 640
 Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr
 645 650 655
 Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro
 660 665 670
 Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala
 675 680 685
 Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser
 690 695 700

Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala
 705 710 715 720
 Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala
 725 730 735
 Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp
 740 745 750
 Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp
 755 760 765
 Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
 770 775 780
 Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
 785 790 795 800
 Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Phe Ser Ile
 805 810 815
 Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
 820 825 830
 Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
 835 840 845
 Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
 850 855 860
 Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
 865 870 875 880
 Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
 885 890 895
 Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val
 900 905 910
 Lys Pro Ile Tyr Phe His Thr Gln
 915 920

<210> 22
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 22
 Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser Ile
 1 5 10

<210> 23
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23
 His Pro Thr His Ser Ser Arg Leu Trp Glu Leu Leu Met Glu Ala Thr
 1 5 10 15
 Pro Thr Met